

GenCore version 5.1.4.p5.4578  
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# OM protein - protein search, using sw model

Run on: April 23, 2003, 12:53:40 ; Search time 14 Seconds  
(without alignments)  
1724 230 Million cell updates/sec

Title: US-09-635-949-34

Perfect score: 3289

Sequence: 1 MDPFLIAVLVSSLYLQAAE.....TGRIGLDVSLKKHCSEER 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	406.5	12.4	2871	1	FNBL_BOVIN	P98133 bos taurus
2	402	12.2	1221	1	FNBL_MOUSE	P37889 mus musculus
3	398.5	12.1	2871	1	FNBL_MOUSE	Q61554 mus musculus
4	397.5	12.1	2911	1	FNBL_HUMAN	P35556 homo sapien
5	397	12.1	2907	1	FNBL_MOUSE	Q61555 mus musculus
6	395.5	12.0	2871	1	FNBL_HUMAN	P35555 homo sapien
7	381.5	11.6	1184	1	FNBL_HUMAN	P98095 homo sapien
8	371	11.3	2671	1	FNBL_PIG	Q9TV36 sus scrofa
9	353.5	10.7	443	1	FNBL_HUMAN	Q95967 homo sapien
10	346.5	10.5	443	1	FNBL_CRICR	O55058 cricetus
11	343	10.4	703	1	FNBL_HUMAN	P23142 homo sapien
12	333.5	10.1	684	1	FNBL_CHICK	O73775 gallus gall
13	332.5	10.1	443	1	FNBL_MOUSE	Q9WVJ9 mus musculus
14	332	10.1	705	1	FNBL_MOUSE	Q98879 mus musculus
15	330.5	10.0	448	1	FNBL_MOUSE	Q9WVH9 mus musculus
16	330.5	10.0	448	1	FNBL_RAT	Q9WVH8 rattus norv
17	329	10.0	835	1	CD97_HUMAN	P48960 homo sapien
18	327	9.9	652	1	CD93_HUMAN	Q9NPY3 homo sapien
19	327	9.9	956	1	FNBL_HUMAN	O00339 homo sapien
20	326.5	9.9	448	1	FNBL_HUMAN	Q9UBX5 homo sapien
21	325	9.9	712	1	FNBL_CAEEL	O77469 caenorhabdi
22	322.5	9.8	956	1	FNBL_MOUSE	O08746 mus musculus
23	314.5	9.6	2556	1	FNBL_HUMAN	P46531 homo sapien
24	311	9.5	1403	1	NID2_MOUSE	O88322 mus musculus
25	310.5	9.4	2524	1	NOTC_XENLA	P21783 xenopus lae
26	308	9.4	2531	1	FNBL_MOUSE	Q01705 mus musculus
27	306.5	9.3	1247	1	FNBL_HUMAN	P14543 homo sapien
28	301	9.2	493	1	FNBL_RAT	O35568 rattus norv
29	297	9.0	2531	1	FNBL_RAT	Q07008 rattus norv
30	296	9.0	1712	1	FNBL_RAT	Q00918 rattus norv
31	295.5	9.0	1394	1	FNBL_HUMAN	P22064 homo sapien
32	295.5	9.0	1595	1	FNBL_HUMAN	Q14766 homo sapien
33	295	9.0	493	1	FNBL_HUMAN	Q12805 homo sapien

## ALIGNMENTS

### RESULT 1

FNBL\_BOVIN STANDARD; PRT: 2871 AA.

AC P98133:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Fibrillin 1 precursor (MP340).

GN FNBL.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

FX MEDLINE=95137597; PubMed=7835900;

KA Tilstra D.J., Potter K.A., Myers P.H.;

RT "Sequence of the coding region of the bovine fibrillin cDNA and

RT localization to bovine chromosome 10.;"

RL Genomics 23:480-485(1994).

RN [2]

RP PARTIAL SEQUENCE.

RX MEDLINE=96132851; PubMed=8557636;

RA Gibson M.A., Hatzinikolas G., Kumaratilake J.S., Sandberg L.B.,

RA Nicholl J.K., Sutherland G.R., Cleary E.G.;

RT "Further characterization of proteins associated with elastic fiber

RT microfibrils including the molecular cloning of MAGP-2 (MP25).;"

RL J. Biol. Chem. 271:1096-1103(1996).

CC !- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS

CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE

CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.

CC !- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER

CC MICROFIBRILS.

CC !- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.

CC !- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.

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CC EMBL: L28748; AAA74122.1; ..

DR HSSP: P35555; IAPJ

DR InterPro: IPR000152; Asx\_hydroxyl.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR001881; EGF\_Ca.

DR InterPro: IPR001438; EGF\_II.

DR InterPro: IPR002212; Fibrill-assoc.

DR Pfam: PF00008; EGF; 46.

DR Pfam: PF00683; TB; 9.

[illegible]





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FT DOMAIN 1648 1688 EGF-LIKE 28, CALCIUM-BINDING.
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FT DOMAIN 1766 1807 EGF-LIKE 29, CALCIUM-BINDING.
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FT DOMAIN 1973 2012 EGF-LIKE 34, CALCIUM-BINDING.
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Query Match 12.1%; Score 398.5; DB 1; Length 2871;
Best Local Similarity 31.7%; Pred. No. 1.4e-15;
Matches 104; Conservative 33; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVG-----GRIDCCGNGARQSWGQCQPPYVLRQRIARI-----RCOLKAVCQPRCKHG 84
DB 1123 LCRGGICHTGTYRC-----ECPPGQLSPNISACIDINECELSA---NLCPHG 1169
QY 85 EC---IGPNKCKCHPCYACK---TCIOVLNKGKIPKPKHRCNMNTYGSYKCYCLNGYM 137
DB 1170 RCVNIIGKYQCACNPGYHPTDRLEFCVDI-DKCSLMNGGCTFTCTNSDGSVECSQCPGFA 1228
QY 138 LMPD-GSCSSALTC--SMANGCYG-CDVVKGQIRQCPSGLQAPDGRVYDV----- 187
DB 1229 LMPDGRSCTDIDQCEENPNICDGGGCTNIPGEYKICG-YDGFMAHSDMKTCVDVNECDLN 1287
QY 188 -----DKCATGRASCPHRCQVNTFGSYI 211
DB 1288 PNICLSGTCENTKGSFICHCDMGYSKKGKTKCTDINECEIGHNKGRIHVAUCTNTAGSEK 1347
QY 212 CKCHKGFIDIMYIGGKYQCHDIDECSLGOYOCSSPFCNVKSCYKCKCKGCGGGLTCV 271
DB 1348 CSCSPG---WIGDGKCTDIDECSTHMGCSHADCKNTMGSYKCLCKDGYTGDFGCT 1403
QY 272 YIPKVMIEPSGPIHVPKNGTILKGDG 299
DB 1404 DLD---ECSENLNL-CGNGQLNAPG 1426

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RESULT 4  
 FBW2 HUMAN STANDARD: PRT: 2911 AA.  
 AC P35556;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-FEB-1996 (Rel. 33, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Fibrillin 2 precursor.  
 GN FBW2.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-941615150; PubMed-8120105;  
 RA Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguinetti C.,  
 RA Bonadio J., Mechem R.P., Ramirez F.;  
 RT "Structure and expression of fibrillin-2, a novel microfibrillar  
 RT component preferentially located in elastic matrices";  
 RL J. Cell Biol. 124:855-863(1994).  
 RN [2]  
 RN SEQUENCE OF 752-1505 FROM N.A.  
 RX MEDLINE-91304567; PubMed-1852206;  
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,  
 RA Tsipouras P., Ramirez F., Hollister D.;  
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to  
 RT two different fibrillin genes";  
 RL Nature 352:330-334(1991).  
 RN [3]  
 RN VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964.  
 RX MEDLINE-96083599; PubMed-7493032;  
 RA Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;  
 RT "Fibrillin-2 (FBW2) mutations result in the Marfan-like disorder,  
 RT congenital contractual arachnodactyly";  
 RL Nat. Genet. 11:456-458(1995).  
 RN [4]  
 RN VARIANTS CCA HIS-1114.  
 RX MEDLINE-98407789; PubMed-9737771;  
 RA Babcock D., Gasner C., Francke U., Maslen G.;  
 RT "A single exon skipping that results in an asp-to-his substitution and  
 RT partial exon skipping in a family with congenital contractual  
 RT arachnodactyly";  
 RL Hum. Genet. 103:22-28(1998).  
 RN [5]  
 RN VARIANTS CCA PHE-1141 AND TRP-1252.  
 RX MEDLINE-20259236; PubMed-10797416;  
 RA Reiche S., Zhou G., Wang M., Der Kaloustian V.M., Pagon R.A.,  
 RA Godfrey M.;  
 RT "Two novel fibrillin-2 mutations in congenital contractual  
 RT arachnodactyly";  
 RL Am. J. Med. Genet. 92:7-12(2000).  
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
 CC THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE  
 CC THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.  
 CC -1- DISEASE: DEFECTS IN FBW2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL  
 CC ARACHNOACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS  
 CC PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT AFFECT THE  
 CC AORTA AND THE EYES.  
 CC -1- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U03272; AAA18950.1;  
 CC EMBL: X62009; -; NOT\_ANNOTATED\_CDS.  
 DR  
 DR PIR: S17063; S17063.  
 DR PIR: S31101; S31101.  
 DR HSSP: P35555; 1EMN.  
 DR Genew: HGNC:3604; FBW2.  
 DR MIM: 121050; -.  
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 DR InterPro: IPR001438; EGF\_II.  
 DR InterPro: IPR002212; Fibrill-assoc.  
 DR Pfam: PF00008; EGF; 45.  
 DR Pfam: PF00683; FN; 9.  
 DR PRINTS: PR00010; EGFHLOOP.  
 DR SMART: SM00179; EGF\_CA; 43.  
 DR SMART: SM00001; EGF\_Like; 3.  
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 DR PROSITE: PS00022; EGF\_1; 2.  
 DR PROSITE: PS01186; EGF\_2; 37.  
 DR PROSITE: PS01187; EGF\_CA; 42.  
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 KW Repeat; Signal; Multigene family; Disease mutation; Polymorphism.  
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Query Match 12.1% Score 397.5; DB 1; Length 2911;  
 Best local similarity 35.0%; Pred. No. 1.6e-15;  
 Matches 84; Conservative 31; Mismatches 72; Indels 53; Gaps 9;

QY 81 CKNGEC---IGPNKKCHPGYAG-----KTCIQVNEGLKRPCKHRCNMTYGVSKCYCL 133  
 DB 1210 CRNGKVNMTGTYQSCNFGYQATPDQGGCTDI-DCMLMNGGCTQCTNSEGSYECSCS 1268  
 QY 134 NGYIMHPDG-SCSSALTC--SMANCOYG-CDVVKGQIRQCPSGLQLAPDRTCVDDVF 189  
 DB 1269 EGYALMPDGRSCADIDECENNPDCDGGGCTNIPGEYRCLC-YDGFMSNDMKTKCIDVNE 1327  
 QY 190 CATGRACPRFCOVNTFGSYCKCHKGFDM----- 221  
 DB 1328 CDLNSNIC-WFGEENWTKGSFICHOLGLYSVKVKGTTGCTDIDVDCRFGAHCNDMHASCLNI 1386

QY 222 -----YIGCKYQCHDIDECISLQYQCSHPARCVNRVGSYKCKKKGYYQDGLTC 270  
 DB 1387 PGSEKCSREGWIGNGIRKIDIDECNSGTHQCSINAQCVNTPGSYRCACSEGTGDTGFTC 1446

RESULT 5  
 FN2\_MOUSE  
 ID FN2\_MOUSE STANDARD: PRT: 2907 AA.  
 AC Q61555; Q63957;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 2 precursor.  
 GN FN2 OR FN2-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP MEDLINE FROM N.A.  
 RX MEDLINE=95263670; PubMed=7744963;  
 RA Zhang H., Hu W., Ramirez F.;  
 RT "Developmental expression of fibrillin genes suggests heterogeneity  
 of extracellular microfibrils.";  
 RL J. Cell Biol. 129:1165-1176(1995).  
 RN [2]  
 RP MEDLINE OF 210-317 FROM N.A.  
 RX MEDLINE=94140368; PubMed=8307578;  
 RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
 Francke U.;  
 RT "Fibrillin genes map to regions of conserved mouse/human synteny on  
 mouse chromosomes 2 and 18.";  
 RL Genomics 18:667-672(1993).  
 CC - FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
 CC - LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
 CC - SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.  
 CC - SIMILARITY: CONTAINS 47 TGF-BETA BINDING PROTEIN DOMAINS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))

EMBL: L39790; AAA74908.1;  
 EMBL: S69359; AAC60665.1;  
 HSP: P35555; IEN.  
 MGI: MGI:95490; Fbn2.  
 InterPro: IPR000152; Asx\_hydroxyl.  
 InterPro: IPR000561; EGF-like.  
 InterPro: IPR001881; EGF-Ca.  
 InterPro: IPR001438; EGF-11.  
 InterPro: IPR002212; Fibril-assoc.  
 Pfam: PF00683; TB: 9.  
 PRINTS: P80010; EGFRILOD.  
 SMART: SM00179; EGF\_CA; 43.  
 SMART: SM00001; EGF\_Like; 3.  
 PROSITE: PS00010; ASX\_HYDROXYL; 43.  
 PROSITE: PS00022; EGF\_1; 2.  
 PROSITE: PS01186; EGF\_2; 36.  
 PROSITE: PS01187; EGF\_CA; 43.  
 Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
 Repeat; Signal; Multigene family.  
 SIGNAL 1 28 POTENTIAL.  
 CHAIN 29 2907 FIBRILLIN 2.  
 DOMAIN 111 142 EGF-LIKE 1.  
 DOMAIN 145 176 EGF-LIKE 2.  
 DOMAIN 176 208 EGF-LIKE 3.

FT DOMAIN 276 317 EGF-LIKE 4, CALCIUM-BINDING.  
 FT REPEAT 318 359 EGF-LIKE 5, CALCIUM-BINDING.  
 FT REPEAT 360 426 TGFHP 1.  
 FT DOMAIN 487 527 EGF-LIKE 6.  
 FT DOMAIN 528 567 EGF-LIKE 7, CALCIUM-BINDING.  
 FT DOMAIN 568 609 EGF-LIKE 8, CALCIUM-BINDING.  
 FT DOMAIN 610 650 EGF-LIKE 9, CALCIUM-BINDING.  
 FT DOMAIN 651 691 EGF-LIKE 10, CALCIUM-BINDING.  
 FT REPEAT 692 760 TGFHP 2.  
 FT DOMAIN 761 802 EGF-LIKE 11, CALCIUM-BINDING.  
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 FT REPEAT 990 1065 TGFHP 3.  
 FT DOMAIN 1066 1107 EGF-LIKE 15, CALCIUM-BINDING.  
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 FT DOMAIN 1525 1565 EGF-LIKE 26, CALCIUM-BINDING.  
 FT REPEAT 1566 1642 TGFHP 4.  
 FT DOMAIN 1643 1684 EGF-LIKE 27, CALCIUM-BINDING.  
 FT DOMAIN 1685 1726 EGF-LIKE 28, CALCIUM-BINDING.  
 FT REPEAT 1727 1800 TGFHP 5.  
 FT DOMAIN 1801 1842 EGF-LIKE 29, CALCIUM-BINDING.  
 FT DOMAIN 1843 1884 EGF-LIKE 30, CALCIUM-BINDING.  
 FT DOMAIN 1885 1926 EGF-LIKE 31, CALCIUM-BINDING.  
 FT DOMAIN 1927 1965 EGF-LIKE 32, CALCIUM-BINDING.  
 FT DOMAIN 1966 2008 EGF-LIKE 33, CALCIUM-BINDING.  
 FT DOMAIN 2009 2048 EGF-LIKE 34, CALCIUM-BINDING.  
 FT DOMAIN 2049 2090 EGF-LIKE 35, CALCIUM-BINDING.  
 FT REPEAT 2091 2163 TGFHP 6.  
 FT DOMAIN 2164 2205 EGF-LIKE 36, CALCIUM-BINDING.  
 FT DOMAIN 2206 2245 EGF-LIKE 37, CALCIUM-BINDING.  
 FT DOMAIN 2246 2286 EGF-LIKE 38, CALCIUM-BINDING.  
 FT DOMAIN 2287 2330 EGF-LIKE 39, CALCIUM-BINDING.  
 FT DOMAIN 2331 2372 EGF-LIKE 40, CALCIUM-BINDING.  
 FT REPEAT 2373 2441 TGFHP 7.  
 FT DOMAIN 2442 2483 EGF-LIKE 41, CALCIUM-BINDING.  
 FT DOMAIN 2484 2524 EGF-LIKE 42, CALCIUM-BINDING.  
 FT DOMAIN 2525 2563 EGF-LIKE 43, CALCIUM-BINDING.  
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 FT DOMAIN 2688 2727 EGF-LIKE 47, CALCIUM-BINDING.  
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 FT DISULFID 132 141 BY SIMILARITY.  
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 FT DISULFID 1696 1710 BY SIMILARITY.  
 FT DISULFID 1712 1725 BY SIMILARITY.

Query Match 12.18; Score 397; DB 1; Length 2407;

Best Local Similarity 39.18; Pred. No. 1.7e-15;

Matches 79; Conservative 33; Mismatches 74; Indels 16; Gaps 9;

QY 81 CKBGECC---IGFNKKCKIIPGYAG---KTCIQVLENGHKKPCKRRCMTYGSYKCYCL 133

DB 1204 CNGKCVNMIGTYGCSNPGYQATPRGCTDI-DKCMIMNGSCMOCNTNSBSYDSGS 1262

QY 134 NGYMLMPDG-SCSSALTC--SMANQYQ-CDVVKYKCPGLQALPRTVDDVLR 189



Db 1263 EGYALPHXGRSCADIDECENNPDI CDGGCTNIPGFRCLC-YDGPMSMDMKTCIDVNE 1321

QY 190 CATGRASCRPRFCVNTFSYICKKHGFDLMYIGKYCHDIDESLGQYQCSSPARYC 249

Db 1322 CDLNPNIC-MFGECENTKGSFICHCQGYSVK--KGTGTCTDVDECEIGHNCDMHASCL 1378

QY 250 NVKGSYKCKCKEYOGDGLTCV 271

Db 1379 NVPSEKSCREGWVGNGIKCI 1400

RESULT 6

ID	FNH1_HUMAN	STANDARD;	PRT; 2871 AA.
AC	P35555;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Fibrillin 1 precursor.		
CN	FNH1 OR FNH1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SOURCE FROM N.A.		
RC	TISSUE=Placenta;		
RX	MEDLINE=93372860; PubMed=8364578;		
RA	Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,		
RA	Pangilinan T., Bonadio J.;		
RT	"Genomic organization of the sequence coding for fibrillin, the		
RT	defective gene product in Marfan syndrome.";		
RL	Hum. Mol. Genet. 2:961-968(1993).		
RN	[2]		
RP	SEQUENCE OF 1-932 FROM N.A.		
RC	TISSUE=Placenta, and Fibroblast;		
RX	MEDLINE=94010947; PubMed=7691719;		
RA	Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;		
RT	"Fibrillin binds calcium and is coded by cDNAs that reveal a		
RT	multidomain structure and alternatively spliced exons at the 5'		
RT	end.";		
RL	Genomics 17:476-484(1993).		
RN	[3]		
RP	SEQUENCE OF 899-2871 FROM N.A.		
RX	MEDLINE=91304568; PubMed=1852207;		
RA	Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;		
RT	"Partial sequence of a candidate gene for the Marfan syndrome.";		
RL	Nature 352:334-337(1991).		
RN	[4]		
RP	SEQUENCE OF 813-1313 FROM N.A.		
RX	MEDLINE=91304567; PubMed=1852206;		
RA	Lee B., Godfrey M., Vitale E., Horii H., Mattei M.-G., Sarfarazi M.,		
RA	Tsipouras P., Ramirez F., Hollister D.W.;		
RT	"Linkage of Marfan syndrome and a phenotypically related disorder to		
RT	two different fibrillin genes.";		
RL	Nature 352:330-334(1991).		
RN	[5]		
RP	CHARACTERIZATION.		
RX	MEDLINE=91317849; PubMed=1860873;		
RA	Sakai L.V., Keene D.R., Glanville R.W., Bachinger H.P.;		
RT	"Purification and partial characterization of fibrillin, a cysteine-		
RT	rich structural component of connective tissue microfibrils.";		
RL	J. Biol. Chem. 266:14763-14770(1991).		
RN	[6]		
RP	STRUCTURE BY NMR OF 2054-2125.		
RX	MEDLINE=98031893; PubMed=9362480;		
RA	Yuan X., Downing A.K., Knott V., Handford P.A.;		
RT	"Solution structure of the transforming growth factor beta-binding		
RT	protein-like module, a domain associated with matrix fibrils.";		
RL	EMBO J. 16:6659-6666(1997).		
RN	[7]		
RP	STRUCTURE BY NMR OF 2124-2205.		
RX	MEDLINE=96144829; PubMed=8568869;		

RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;

RT "Calcium binding properties of an epidermal growth factor-like domain

RL pair from human fibrillin-1.";

RN J. Mol. Biol. 255:22-27(1996).

RP STRUCTURE BY NMR OF 2124-2205.

RX MEDLINE=96222301; PubMed=8653794;

RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,

RA Handford P.A.;

RT "Solution structure of a pair of calcium-binding epidermal growth

RT factor-like domains: implications for the Marfan syndrome and other

RT genetic disorders.";

RL Cell 85:597-605(1996).

RN [9]

RP REVIEW ON MFS VARIANTS.

RX MEDLINE=96174615; PubMed=8594563;

RA Colod G., Beroud C., Soussi T., Junien C., Boileau C.;

RT "Software and database for the analysis of mutations in the human

RT FNH1 gene.";

RL Nucleic Acids Res. 24:137-141(1996).

RN [10]

RP REVIEW ON MFS VARIANTS.

RX MEDLINE=97169383; PubMed=9016526;

RA Colod-Reroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,

RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,

RA Richards R.I., Wang W., Junien C., Boileau C.;

RT "Marfan Database (second edition): software and database for the

RT analysis of mutations in the human FNH1 gene.";

RL Nucleic Acids Res. 25:147-150(1997).

RN [11]

RP REVIEW ON VARIANTS.

RX MEDLINE=98062175; PubMed=9401003;

RA Hayward C., Brock D.J.H.;

RT "Fibrillin-1 mutations in Marfan syndrome and other type-1

RT fibrillinopathies.";

RL Hum. Mutat. 10:415-423(1997).

RN [12]

RP VARIANT MFS PRO-1137.

RX MEDLINE=91304569; PubMed=1852208;

RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,

RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,

RA Curristin S.M., Stetten G., Meyers D.A., Francomano C.A.;

RT "Marfan syndrome caused by a recurrent de novo missense mutation in

RT the fibrillin gene.";

RL Nature 352:337-339(1991).

RN [13]

RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.

RX MEDLINE=93250834; PubMed=1301946;

RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;

RT "Clustering of fibrillin (FNH1) missense mutations in Marfan syndrome

RT patients at cysteine residues in EGF-like domains.";

RL Hum. Mutat. 1:366-374(1992).

RN [14]

RP VARIANT MFS SPR-2307.

RX MEDLINE=92235290; PubMed=1569206;

RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,

RA Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;

RT "Marfan phenotype variability in a family segregating a missense

RT mutation in the epidermal growth factor-like motif of the fibrillin

RT gene.";

RL J. Clin. Invest. 89:1674-1680(1992).

RN [15]

RP VARIANTS MFS ILE-548 AND ALA-723.

RX MEDLINE=94010946; PubMed=8406497;

RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,

RA Pyeritz R.E., Francomano C.A.;

RT "Four novel FNH1 mutations: significance for mutant transcript level

RT and EGF-like domain calcium binding in the pathogenesis of Marfan

RT syndrome.";

RL Genomics 17:468-475(1993).

RN [16]

RP VARIANTS MFS SER-2144.

RX MEDLINE=93278402; PubMed=8504310;

RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.:  
 RT "A novel fibrillin mutation in the Marfan syndrome which could  
 RL disrupt calcium binding of the epidermal growth factor-like module.";  
 RN Hum. Mol. Genet. 2:475-477(1993).  
 RP VARIANTS MFS R-862; Y-1117; P-1137 AND F-1589, AND VARIANT A-1148.  
 RX MEDLINE-94108431; PubMed-8281141;  
 RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gasner C.,  
 RA Borg M.A., Miller D.C., Francke U.:  
 RT "Mutation screening of complete fibrillin-1 coding sequence: report  
 RL of five new mutations, including two in B-cysteine domains.";  
 RN Hum. Mol. Genet. 2:1813-1821(1993).  
 RP VARIANTS MFS GLY-217 AND ARG-2627.  
 RX MEDLINE-95067970; PubMed-7977366;  
 RA Karttunen L., Raghunath M., Leenqvist L., Peltonen L.:  
 RT "A compound-heterozygous Marfan patient: two defective fibrillin  
 RL alleles result in a lethal phenotype.";  
 RN Am. J. Hum. Genet. 55:1083-1091(1994).  
 RP VARIANT EL IYS-2447.  
 RX MEDLINE-94245249; PubMed-8188302;  
 RA Leenqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,  
 RA Peltonen L.:  
 RT "A novel mutation of the fibrillin gene causing ectopia lentis.";  
 RL Genomics 19:573-576(1994).  
 RP VARIANT MFS CYS-627.  
 RX MEDLINE-94272487; PubMed-8004112;  
 RA Hayward C., Rae A.B., Porteous M.E.M., Loeig L.J., Brock L.J.:  
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains  
 RL of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan  
 RN syndrome patients.";  
 RP Hum. Mol. Genet. 3:373-375(1994).  
 RP VARIANT MFS CYS-122.  
 RX MEDLINE-94314977; PubMed-8040326;  
 RA Stahl-Hallenqren C., Ukkonen T., Kainulainen K., Kristofersson U.,  
 RA Saxne T., Tornqvist K., Peltonen L.:  
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth  
 RL factor-like motifs of the FBN1 polypeptide is connected to a novel  
 RN variant of Marfan syndrome.";  
 RP J. Clin. Invest. 94:709-713(1994).  
 RP VARIANT MFS TYR-1223.  
 RX MEDLINE-94351682; PubMed-8071963;  
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.:  
 RT "A new missense mutation of fibrillin in a patient with Marfan  
 RL syndrome.";  
 RN J. Med. Genet. 31:338-339(1994).  
 RP VARIANT MFS HIS-1170.  
 RX MEDLINE-95174777; PubMed-7870075;  
 RA Hayward C., Porteous M.E.M., Brock D.J.H.:  
 RT "A novel mutation in the fibrillin gene (FBN1) in familial  
 RL arachnodactyly.";  
 RN Mol. Cell. Probes 8:325-327(1994).  
 RP VARIANTS MFS G-217; N-1023; R-1074; Y-1242; R-1513; E-2127; W-2151;  
 RX K-2447 AND R-2511.  
 RA MEDLINE-94184368; PubMed-8136837;  
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.:  
 RT "Mutations in the fibrillin gene responsible for dominant ectopia  
 RL lentis and neonatal Marfan syndrome.";  
 RN Nat. Genet. 6:64-69(1994).  
 RP VARIANT SER-1127.  
 Query Match 12.0%; Score 395.5; DH 1; Length 2871;  
 Best local Similarity 31.4%; Pred. No. 2.1e-15;  
 Matches 103; Conservative 34; Mismatches 104; Indels 87; Gaps 15;  
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DB 1123 LCRGGVCHINTEGYSRC-----ECPGHIQSPNISACIDINEELSA---BLCPNG 1169  
 QY 85 EC---IGPNKCKHCPCYACKT-----CLOVNFPGCLPKPCCKHRCWNTYCYKYCGLNGYM 137  
 DB 1170 RCVNLEIGKYOCACNPGYHSTPDLKFCVDI-DEGSMNGGCTETCTNSESGSYESGCGGPA 1228  
 QY 138 LMPD-GCSCSSALTG--SMANCOVG-CDVVKGQIRGCFSPGLQALAFDRTVDV--- 187  
 DB 1229 LMPDQASCDIIDECHNPNI CDGGCQCTNIPGHCRLC-YDGFWASHDKKTCVIVNEDTLN 1287  
 QY 188 -----DECATGRASVPRFRQVNTFSSVI 211  
 DB 1288 PNICLSGTGENTKSGPICHGDMGYSKKGKTGCTDINEGEIGAHNCGKIAVCTNTAGSEK 1347  
 QY 212 CCKHCKGFDLMYIGGKYOCCHDIOPCSLGOYCSPANCYVNRGSKCKCKGKYOCGLFV 271  
 DB 1348 CSCSPG---WIGDGIKCTDDECSNGTMCQIADKNTMGSYRGLKREGYTGKHTT 1403  
 QY 272 YIPKVMIEPSGPIHVPKNGNTILKGDG 299  
 DB 1404 DLD-ECSENLM-CCGNCQCLNAICG 1426  
 ID FBL2.HUMAN STANDARD; PRT; 1184 AA.  
 AC P98095;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fibrillin-2 precursor.  
 GN FBLN2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 SKQFNCE FROM N.A.  
 RC TISSUE-Fibroblast;  
 RX MEDLINE-95104855; PubMed-7806230;  
 RA Zhang R.-Z., Fan T.-C., Zhang Z.-Y., Mattei M. G., Timpi K.,  
 RA Chu M.-L.;  
 RT "Fibrillin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping  
 RL of the gene on human and mouse chromosomes.";  
 CC Genomics 22:425-430(1994).  
 CC 1- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS  
 CC CALCIUM DEPENDENT.  
 CC 1- SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED.  
 CC 1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX. COMPONENT OF BOTH  
 CC HASHNET MEMBRANES AND OTHER CONNECTIVE TISSUES.  
 CC 1- TISSUE SPECIFICITY: EXPRESSED IN HEART, PLACENTA AND OVARY.  
 CC 1- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.  
 CC 1- SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.  
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 DR FMHL; X82494; CAA57876.1;  
 DR HSSP; P00736; IAPQ.  
 DR Genew; IGNC:3601; FBLN2.  
 DR MIM: 135821;  
 DR InterPro; IPR000020; Anaphylatoxin.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00608; EGF; 7.  
 DR Pfam; PF01821; ANATO; 2.







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DB 135 --RVSQD--CHNLPGSYGCTCHDGRKIGPK--CVDIDECRYRYCQHRKCVNI.PGSFRCOC- 188
QY 172 SPGLQADGRTGVDVDECATGRASCPFRPQCYNTGSGYCKHGKGFDLMYIGSKYQCHD 231
DB 189 EPGHQLGPNKRSVDNFECDMG--AICWQRCVNSVGTPLCRCHQGYELHRDG--PSCSD 243
QY 232 IDECSLQYQYCCSFARCVNRYGSKCKCKGQY-----GNGHGTGV 271
DB 244 IDECSYSSYLQY--YRCVNEPGRFSCHKPGQYQLLATRLCQIDECESHAHQCSAQTCV 301
QY 272 YIPKVMIEPSPHVPKGNCTIILKDTGNANNWIDVGSSTWHPKTPYIPVITNR---PT 328
DB 302 NF-----HOCYRCVDIF--NRCV-----EPYI-QVSNRRCICPA 331
QY 329 SKPTTRTPKPTPIPTPPPPPTLPLPTTPTTPTTGLTIAPMASTPPGGITVD 368
DB 332 SNPLCRQ-----PSSIVHRYMTITSRSVPADVFOIQAISVYPGAY--- 373
QY 389 NRVTIDPKPRGVDVFIPIQPSN 410
DB 374 NAFQIRAGNSQGFYI-ROINN 394

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RESULT 10
FBL4_CRIGR STANDARD; PRT; 443 AA.
AC 025058;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
DE (Fibulin-4) (FBLN-4) (H411 protein).
GN EFEMP2 OR FBLN4.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Heine H., Delude R.L., Monks B., Golenbock D.T.;
RI Submitted (FEH-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch.)
CC -----
CC EMBL: AF046870; AAC03101.1;
CC DR HISSP; P00736; IAPQ.
CC DR InterPro: IPR000152; Asx_hydroxyl.
CC DR InterPro: IPR000561; EGF-like.
CC DR InterPro: IPR001881; EGF_Ca.
CC DR Pfam: PRD0008; EGF_4.
CC DR SMART: SM00179; EGF_CA; 4.
CC DR SMART: SM00001; EGF-like; 2.
CC DR PROSITE: PS00010; ASX_HYDROXYL; 4.
CC DR PROSITE: PS00022; EGF_1; FALSE_NEG.
CC DR PROSITE: PS01186; EGF_2; 4.
CC DR PROSITE: PS01187; EGF_CA; 6.
CC Repeat: EGF-like domain; Calcium-binding; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CCHAIN 26 443
FT FT
FT DOMAIN 36 81
FT FT
FT DOMAIN 123 163
FT FT

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FT DOMAIN 164 202
FT DOMAIN 203 242
FT DOMAIN 243 282
FT DOMAIN 283 328
FT DISULFID 127 140
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FT DISULFID 151 162
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FT DISULFID 173 186
FT DISULFID 188 201
FT DISULFID 207 217
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FT DISULFID 228 241
FT DISULFID 247 258
FT DISULFID 254 267
FT DISULFID 269 281
FT DISULFID 287 300
FT DISULFID 294 309
FT DISULFID 315 327
FT CARBOHYD 198
FT CARBOHYD 394
SQ SEQUENCE 443 AA; 49432 MW; 0BCE5D732D9E5F CRC64;
Query Match 10.5%; Score 346.5; DH 1; Length 443;
Best Local Similarity 36.8%; Pred. No. 2, Ho-13;
Matches 77; Conservative 31; Mismatches 68; Indels 44; Gaps 12;
QY 76 VCPGCK-----HGEICGP-----NKCKCPGY---AGKTCIGVLNEGCLKPKPK 118
DB 79 LCUPRRAAVINDIHRG--GPPPPVPPAHHNPPPPPPPPPPPPPPPPPPPPPPPPPP 135
QY 119 --HRCNTYGSYKCYGKCYGKCYGKCYGKCYGKCYGKCYGKCYGKCYGKCYGKCYG 175
DB 136 PSQDCHNLPGSYGCTCPDGYRKGPE--CVDIDECRYRYCQHRKCVNI.PGSFRCOC 192
QY 176 OLAPDGHCTVDVDECATGRASCPFRPQCYNTGSGYCKHGKGFDLMYIGSKYQCHD 235
DB 193 OLGPNNRSVDNFECDMG---AICWQRCVNSVGTPLCRCHQGYELHRDG--PSCSD 247
QY 236 SLGQYCCSFARCVNRYGSKCKCKGQY 264
DB 248 SYSSYLQY--YRCVNEPGRFSCHKPGQY 274
RESULT 11
FBL1_HUMAN STANDARD; PRT; 703 AA.
AC P23142; P23143; P23144; P37888; Q90GR4;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibulin-1 precursor.
GN FBLN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RX MEDLINE-91100426; PubMed-2269669;
RA Argraves W.S., Tran H., Hargess W.H., Dickerson K.;
RT *Fibulin is an extracellular matrix and plasma glycoprotein with
RT repeated domain structure.*
RL J. Cell Biol. 111:3155-3164(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM D).
RA Argraves S.;
RN Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 567-703 FROM N.A. (ISOFORM C).
RA Connor R.;
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]

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RP SEQUENCE OF 30-44.  
 RA MEDLINE:89354537; PubMed-2527614;  
 RA Agraves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;  
 RT "Fibulin, a novel protein that interacts with the fibronectin  
 RL receptor beta subunit cytoplasmic domain."; Cell 58:623-629(1989).  
 CC -!- SUPRACELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A, B, C AND D (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER ONLY IN THEIR C-  
 CC TERMINAL REGIONS.  
 CC -!- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.  
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 DR EMBL: X53741; CAA37770.1; -  
 DR EMBL: X53742; CAA37771.1; -  
 DR EMBL: X53743; CAA37772.1; -  
 DR EMBL: U01244; AAH17099.1; -  
 DR EMBL: Z95331; CAB62360.1; -  
 DR PIR: A32826; A32826.  
 DR PIR: A36346; A36346.  
 DR PIR: B36346; B36346.  
 DR PIR: C36346; C36346.  
 DR HSSP: P35555; 1PMN.  
 DR Genew: HGNC:3600; FBLN1.  
 DR MIM: 135820; -  
 DR InterPro: IPR000020; Anaphylatoxin.  
 DR SMART: SM00104; ANATO; 3.  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_CA.  
 DR Pfam: PF00008; EGF; 6.  
 DR Pfam: PF01821; ANATO; 3.  
 DR SMART: SM00179; EGF\_CA; 7.  
 DR SMART: SM00001; EGF\_Like; 2.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 4.  
 DR PROSITE: PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE: PS01177; ANAPHYLATOXIN\_1; 3.  
 DR PROSITE: PS01178; ANAPHYLATOXIN\_2; 3.  
 DR PROSITE: PS01186; EGF\_2; 3.  
 DR PROSITE: PS01187; EGF\_CA; 8.  
 KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;  
 KW Repeat; EGF-like domain; Calcium-binding.  
 FT SIGNAL 1 29  
 FT CHAIN 30 703 FIBULIN-1.  
 FT DOMAIN 36 76 ANAPHYLATOXIN-LIKE 1.  
 FT DOMAIN 77 111 ANAPHYLATOXIN-LIKE 2.  
 FT DOMAIN 112 144 ANAPHYLATOXIN-LIKE 3.  
 FT DOMAIN 176 215 EGF-LIKE 1.  
 FT DOMAIN 216 261 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 262 307 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 308 355 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 356 398 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 399 440 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 441 480 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 481 524 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 525 578 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).  
 FT DISULFID 36 61 BY SIMILARITY.  
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 FT DISULFID 50 69 BY SIMILARITY.  
 FT DISULFID 78 109 BY SIMILARITY.  
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 FT DISULFID 556 577 BY SIMILARITY.  
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 FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 539 539 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 567 703 MISSING (IN ISOFORM A).  
 FT VARSPLIC 567 601 LQEKTDTRCICRSKRPNDVTCVDPVHTISHIVI -> OK  
 SKKQKNIPAGSKEDCKVLPMKQGLDTHIDA (IN  
 ISOFORM B).  
 FT VARSPLIC 567 703 LQEKTDTRCICRSKRPNDVTCVDPVHTISHIVI  
 EFTPEELIFLRAITPPASQANIIFDTEGNLRDSEFII  
 KRYMDGTVGVRVQVPIVGFHAYKLHNNYVGVVSHR  
 NVNVRIFVSYWF -> NCHRLCHENNRCSKULRITTY  
 HUSPTNTQAPVFRMPGSAVPCDSMQIAITGNGFPGFF  
 TTRKVSHPGVAULTKVPPEPROLLTVKMDLSRHGTVSF  
 VAKLFIYSAEL (IN ISOFORM C).  
 FT CONFLICT 36 36 HR -> SH (IN REF. 4).  
 FT CONFLICT 41 42  
 FT SEQUENCE 703 AA; 77274 MW; EFD88465BA2D3A25 CRC64;  
 Query Match 10.4%; Score 343; DB 1; Length 703;  
 Best Local Similarity 26.7%; Pred. No. 6.4e-13;  
 Matches 106; Conservative 43; Mismatches 118; Indels 130; Gaps 20.  
 QY 31 SSIGLCRYGGRIDCCGWAKRSWGQC-----QPFYVLKQRIAR 68  
 DB 281 NTLGSFRCPKLOCKSGFIQDAGLNCIDINECLISAPCPIGHTCINTEGSYTCOKNVPN 340  
 QY 69 -----IRCOLKAVCOP---RCKHG-ECI---GPNCKCKHPGY---AGTKCIQV 106  
 DB 341 CGRGYHINEGTRCVDDVDECAPPAPCGKHGKCVNSPGFCECKTGTYFPGISNMCVIV 400  
 QY 107 LNECGLKP-RPCKHRCMNTYSGYKCYCLNGYMLMPDG-SCSSALTCSSMANCYGCDVYVK 164  
 DB 401 -NECQYFGRCLGHKCENTLGSYLCSCSVGPRLSVDGRSCEDINECSSPSCQCANVYG 459  
 QY 165 QIRQCPSPIQLAP-DGRTCVDDVDECA--TCRASCPHFQCVNTFGSYICKC-HKGDPI. 220  
 DB 460 SYQCYC-RRGYOLSDVGVTCEDICALPTGGHLCIS--YRCINIPGFGQSCPSSGYRL 516  
 QY 221 MYIGKYOCHDIDECSLGYQCSSEFARCYNVVRSYKCY---KCKEY----- 263  
 DB 517 APNG--RNCQDIDECVTGIHNCISINETCFNIOGAPCLAPFCPEYKSAATLQOKKWT 574  
 QY 264 -----QDGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWPKPT 316  
 DB 575 VRCIKSRPNDVTCF-----DPVIT----- 595  
 QY 317 PYIPPIITNRPYSKPTTRTPKPTPI-----PTPPP 348









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FT DISULFID 138 153 BY SIMILARITY.
FT DISULFID 155 166 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 177 190 BY SIMILARITY.
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FT DISULFID 273 286 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 299 314 BY SIMILARITY.
FT DISULFID 320 332 BY SIMILARITY.
FT CARBOHYD 283 296 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 448 AA; 50193 MW; F15CC70CCFBDC97 CRG64;

Query Match 10.0%; Score 330.5; DB 1; Length 448;
Best Local Similarity 40.0%; Pred. No. 2.3e-12;
Matches 70; Conservative 18; Mismatches 72; Indels 15; Gaps 8;

QY 94 CHPGY---AGKTCIQVLNEGGLKPRCK--HRCMNTYGSYKCYCLNGYMIIMPDGSSAL 148
Db 113 CRFGYQNDGEGNOCVDV-DECATDSHCNPTQICINTEGGYTCSTDCGYWLL-EGCCLDID 170

QY 149 TCSMANCOYGDVVKQIRQCPSGLQIAPDGRTCVDVDECATGRASCPRFROCYNTPG 208
Db 171 ECRYGYCQQLCANVPGSYSCTC-NPGFTLNDGRSCQDVNECETEN---PCVQTCVNTYG 226

QY 209 SYICKCHKGFDMYIGGKYCHDIDEGSLGYQCSSFARCYNVYRGSYKCKCKEGY 263
Db 227 SFICRDPGYLEHDX--IHCSDMDECSFSEFLCOH--ECVNQPGSYFCSCPQY 277
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Search Completed: April 23, 2003, 13:01:36  
Job time : 26 secs

